



## RAW SEQUENCE LISTING

DATE: 01/29/2002

PATENT APPLICATION: US/09/645,415A

TIME: 14:21:10

Input Set : A:\8002059999.app

Output Set: N:\CRF3\01292002\I645415A.raw

P.S

ENTERED

```

4 <110> APPLICANT: Bermudes, G.
5   King, I.
6   Clairmont, C.
7   Lin, S.
8   Belcourt, M.
10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
11   TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
14 <130> FILE REFERENCE: 8002-059
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/645,415A
C--> 16 <141> CURRENT FILING DATE: 2000-08-24
16 <150> PRIOR APPLICATION NUMBER: 60/157,581
17 <151> PRIOR FILING DATE: 1999-10-04
19 <150> PRIOR APPLICATION NUMBER: 60/157,637
20 <151> PRIOR FILING DATE: 1999-10-04
22 <160> NUMBER OF SEQ ID NOS: 61
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 26
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Forward primer
34 <400> SEQUENCE: 1
35   gaagatcttc cggaggaggg gaaatg
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 44
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Reverse primer
45 <400> SEQUENCE: 2
46   cgggatccga gctcgagggc cgggaaagg atctaagaag atcc
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 477
50 <212> TYPE: DNA
51 <213> ORGANISM: Homo sapiens
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (1)...(474)
57 <400> SEQUENCE: 3
58   atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat
59   Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
60   1          5          10          15

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```

62 gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt      96
63 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
64      20      25      30
66 cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag      144
67 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
68      35      40      45
70 ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg      192
71 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
72      50      55      60
74 ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc      240
75 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
76      65      70      75      80
78 atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc      288
79 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
80      85      90      95
82 gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg      336
83 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
84      100      105      110
86 aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag      384
87 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
88      115      120      125
90 aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat      432
91 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
92      130      135      140
94 ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg      474
95 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
96      145      150      155
98 taa      477
100 <210> SEQ ID NO: 4
101 <211> LENGTH: 158
102 <212> TYPE: PRT
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 4
106 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
107      1      5      10      15
108 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
109      20      25      30
110 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
111      35      40      45
112 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
113      50      55      60
114 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
115      65      70      75      80
116 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
117      85      90      95
118 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
119      100      105      110
120 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
121      115      120      125

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122 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
123      130      135      140
124 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
125 145      150      155
127 <210> SEQ ID NO: 5
128 <211> LENGTH: 28
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Forward primer
135 <400> SEQUENCE: 5
136 ccgacgcgtt gacacctgaa aactggag 28
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 29
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Reverse primer
146 <400> SEQUENCE: 6
147 ccgacgcgtg aaaggatctc aagaagatc 29
149 <210> SEQ ID NO: 7
150 <211> LENGTH: 543
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Fusion construct
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (1)...(540)
160 <400> SEQUENCE: 7
161 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct 48
162 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
163 1      5      10      15
165 acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc 96
166 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
167      20      25      30
169 gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag 144
170 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
171      35      40      45
173 ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt 192
174 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
175 50      55      60
177 gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg 240
178 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
179 65      70      75      80
181 atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat 288
182 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
183      85      90      95
185 gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc 336
186 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr

```

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Input Set : A:\8002059999.app

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```

187          100          105          110
189 aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act      384
190 Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
191          115          120          125
193 ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt      432
194 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
195          130          135          140
197 ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac      480
198 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
199 145          150          155          160
201 cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt      528
202 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
203          165          170          175
205 att atc gca ctg taa      543
206 Ile Ile Ala Leu
207          180
210 <210> SEQ ID NO: 8
211 <211> LENGTH: 180
212 <212> TYPE: PRT
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Fusion construct
218 <400> SEQUENCE: 8
219 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
220 1 5 10 15
221 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
222 20 25 30
223 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
224 35 40 45
225 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
226 50 55 60
227 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
228 65 70 75 80
229 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
230 85 90 95
231 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
232 100 105 110
233 Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
234 115 120 125
235 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
236 130 135 140
237 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
238 145 150 155 160
239 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
240 165 170 175
241 Ile Ile Ala Leu
242 180
244 <210> SEQ ID NO: 9
245 <211> LENGTH: 801

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TIME: 14:21:11

Input Set : A:\8002059999.app

Output Set: N:\CRF3\01292002\I645415A.raw

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246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Fusion construct
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (1)...(798)
255 <400> SEQUENCE: 9
256 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct 48
257 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
258 1 5 10 15
260 acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac 96
261 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
262 20 25 30
264 aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt 144
265 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
266 35 40 45
268 tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa 192
269 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
270 50 55 60
272 gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc 240
273 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
274 65 70 75 80
276 tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct 288
277 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
278 85 90 95
280 ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act 336
281 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
282 100 105 110
284 ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat 384
285 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
286 115 120 125
288 gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt 432
289 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
290 130 135 140
292 ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc 480
293 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
294 145 150 155 160
296 atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga 528
297 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
298 165 170 175
300 ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc 576
301 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
302 180 185 190
304 caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg 624
305 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
306 195 200 205
308 aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc 672
309 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
310 210 215 220

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 01/29/2002

PATENT APPLICATION: US/09/645,415A

TIME: 14:21:12

Input Set : A:\8002059999.app

Output Set: N:\CRF3\01292002\I645415A.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57

L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59